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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/587,574

DATE: 11/21/2000  
TIME: 15:13:53

Input Set: I587574.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin  
2 <120> TITLE OF INVENTION: Conductine protein and a related agent for diagnosing  
3 and treating tumor illnesses  
4 <130> FILE REFERENCE: 0107-026 US  
5 <140> CURRENT APPLICATION NUMBER: US/09/587,574  
6 <141> CURRENT FILING DATE: 2000-06-05  
7 <150> EARLIER APPLICATION NUMBER: DE 197 38 205.3  
8 <151> EARLIER FILING DATE: 1997-09-02  
9 <160> NUMBER OF SEQ ID NOS: 10  
10 <170> SOFTWARE: PatentIn Ver. 2.1  
11 <210> SEQ ID NO 1  
12 <211> LENGTH: 840  
13 <212> TYPE: PRT  
14 <213> ORGANISM: Artificial Sequence  
15 <220> FEATURE:  
16 <223> OTHER INFORMATION: Description of Artificial Sequence: Conductine  
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23 Thr Pro Pro Cys Gln Pro Ser Val Gly Lys Val Gln Ser Thr Lys Pro  
24 35 40 45  
25 Met Pro Val Ser Ser Asn Ala Arg Arg Asn Glu Asp Gly Leu Gly Glu  
26 50 55 60  
27 Pro Glu Gly Arg Ala Ser Pro Asp Ser Pro Leu Thr Arg Trp Thr Lys  
28 65 70 75 80  
29 Ser Leu His Ser Leu Leu Gly Asp Gln Asp Gly Ala Tyr Leu Phe Arg  
30 85 90 95  
31 Thr Phe Leu Glu Arg Glu Lys Cys Val Asp Thr Leu Asp Phe Trp Phe  
32 100 105 110  
33 Ala Cys Asn Gly Phe Arg Gln Met Asn Leu Lys Asp Thr Lys Thr Leu  
34 115 120 125  
35 Arg Val Ala Lys Ala Ile Tyr Lys Arg Tyr Ile Glu Asn Asn Ser Val  
36 130 135 140  
37 Val Ser Lys Gln Leu Lys Pro Ala Thr Lys Thr Tyr Ile Arg Asp Gly  
38 145 150 155 160  
39 Ile Lys Lys Gln Gln Ile Gly Ser Val Met Phe Asp Gln Ala Gln Thr  
40 165 170 175  
41 Glu Ile Gln Ala Val Met Glu Glu Asn Ala Tyr Gln Val Phe Leu Thr  
42 180 185 190  
43 Ser Asp Ile Tyr Leu Glu Tyr Val Arg Ser Gly Gly Glu Asn Thr Ala  
44 195 200 205

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47	Leu	Pro	Thr	Leu	Asn	Glu	Glu	Glu	Glu	Trp	Thr	Cys	Ala	Asp	Leu	Lys
48	225					230					235					240
49	Cys	Lys	Leu	Ser	Pro	Thr	Val	Val	Gly	Leu	Ser	Ser	Lys	Thr	Leu	Arg
50					245					250					255	
51	Ala	Thr	Ala	Ser	Val	Arg	Ser	Thr	Glu	Thr	Ala	Glu	Asn	Gly	Phe	Arg
52				260					265					270		
53	Ser	Phe	Lys	Arg	Ser	Asp	Pro	Val	Asn	Pro	Tyr	His	Val	Gly	Ser	Gly
54			275					280					285			
55	Tyr	Val	Phe	Ala	Pro	Ala	Thr	Ser	Ala	Asn	Asp	Ser	Glu	Leu	Ser	Ser
56		290					295					300				
57	Asp	Ala	Leu	Thr	Asp	Asp	Ser	Met	Ser	Met	Thr	Asp	Ser	Ser	Val	Asp
58	305					310					315					320
59	Gly	Val	Pro	Pro	Tyr	Arg	Met	Gly	Ser	Lys	Lys	Gln	Leu	Gln	Arg	Glu
60					325					330					335	
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62				340					345					350		
63	Pro	Arg	Thr	His	Arg	Leu	Pro	Lys	Glu	Met	Thr	Pro	Val	Glu	Pro	Ala
64			355					360					365			
65	Ala	Phe	Ala	Ala	Glu	Leu	Ile	Ser	Arg	Leu	Glu	Lys	Leu	Lys	Leu	Glu
66		370					375					380				
67	Leu	Glu	Ser	Arg	His	Ser	Leu	Glu	Glu	Arg	Leu	Gln	Gln	Ile	Arg	Glu
68	385					390					395					400
69	Asp	Glu	Glu	Lys	Glu	Gly	Ser	Glu	Gln	Ala	Leu	Ser	Ser	Arg	Asp	Gly
70					405					410					415	
71	Ala	Pro	Val	Gln	His	Pro	Leu	Ala	Leu	Leu	Pro	Ser	Gly	Ser	Tyr	Glu
72				420					425					430		
73	Glu	Asp	Pro	Gln	Thr	Ile	Leu	Asp	Asp	His	Leu	Ser	Arg	Val	Leu	Lys
74			435					440					445			
75	Thr	Pro	Gly	Cys	Gln	Ser	Pro	Gly	Val	Gly	Arg	Tyr	Ser	Pro	Arg	Ser
76		450					455					460				
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78	465					470					475					480
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84			515					520					525			
85	Ile	Glu	Ala	Glu	Ala	Thr	Gln	Arg	Val	Arg	Cys	Leu	Cys	Pro	Gly	Gly
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87	Thr	Asp	Tyr	Tyr	Cys	Tyr	Ser	Lys	Cys	Lys	Ser	His	Pro	Lys	Ala	Pro
88	545					550					555					560
89	Glu	Pro	Leu	Pro	Gly	Glu	Gln	Phe	Cys	Gly	Ser	Arg	Gly	Gly	Thr	Leu
90					565					570					575	
91	Pro	Lys	Arg	Asn	Ala	Lys	Gly	Thr	Glu	Pro	Gly	Leu	Ala	Leu	Ser	Ala
92				580					585					590		
93	Arg	Asp	Gly	Gly	Met	Ser	Ser	Ala	Ala	Gly	Gly	Pro	Gln	Leu	Pro	Gly
94			595					600					605			

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95      Glu Glu Gly Asp Arg Ser Gln Asp Val Trp Gln Trp Met Leu Glu Ser
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98      625                      630                      635                      640
99      Ser Tyr Pro Leu Glu Ser Ala Arg Ala Ala Pro Gly Glu Arg Val Ser
100          645                      650                      655
101      Arg His His Leu Leu Gly Ala Ser Gly His Ser Arg Ser Val Ala Arg
102          660                      665                      670
103      Ala His Pro Phe Thr Gln Asp Pro Ala Met Pro Pro Leu Thr Pro Pro
104          675                      680                      685
105      Asn Thr Leu Ala Gln Leu Glu Glu Ala Cys Arg Arg Leu Ala Glu Val
106          690                      695                      700
107      Ser Lys Pro Gln Lys Gln Arg Cys Cys Val Ala Ser Gln Gln Arg Asp
108      705                      710                      715                      720
109      Arg Asn His Ser Ala Ala Gly Gln Ala Gly Ala Ser Pro Phe Ala Asn
110          725                      730                      735
111      Pro Ser Leu Ala Pro Glu Asp His Lys Glu Pro Lys Lys Leu Ala Ser
112          740                      745                      750
113      Val His Ala Leu Gln Ala Ser Glu Leu Val Val Thr Tyr Phe Phe Cys
114          755                      760                      765
115      Gly Glu Glu Ile Pro Tyr Arg Arg Met Leu Lys Ala Gln Ser Leu Thr
116          770                      775                      780
117      Leu Gly His Phe Lys Glu Gln Leu Ser Lys Lys Gly Asn Tyr Arg Tyr
118      785                      790                      795                      800
119      Tyr Phe Lys Lys Ala Ser Asp Glu Phe Ala Cys Gly Ala Val Phe Glu
120          805                      810                      815
121      Glu Ile Trp Asp Asp Glu Thr Val Leu Pro Met Tyr Glu Gly Arg Ile
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129      <220> FEATURE:
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136          20                      25                      30
137      Phe Trp Phe Ala Cys Asn Gly Phe Arg Gln Met Asn Leu Lys Asp Thr
138          35                      40                      45
139      Lys Thr Leu Arg Val Ala Lys Ala Ile Tyr Lys Arg Tyr Ile Glu Asn
140          50                      55                      60
141      Asn Ser Val Val Ser Lys Gln Leu Lys Pro Ala Thr Lys Thr Tyr Ile
142          65                      70                      75                      80
143      Arg Asp Gly Ile Lys Lys Gln Gln Ile Gly Ser Val Met Phe Asp Gln
144          85                      90                      95

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150 <211> LENGTH: 54
151 <212> TYPE: PRT
152 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial
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158          1                      5                      10                      15
159      Pro Lys Glu Met Thr Pro Val Glu Pro Ala Ala Phe Ala Ala Glu Leu
160          20                      25                      30
161      Ile Ser Arg Leu Glu Lys Leu Lys Leu Glu Leu Glu Ser Arg His Ser
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168 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial
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172      binding domain)
173 <400> SEQUENCE: 4
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177          20                      25                      30
178      Gly Ser Tyr Glu Glu Asp Pro Gln Thr Ile Leu Asp Asp His Leu Ser
179          35                      40                      45
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185 <211> LENGTH: 51
186 <212> TYPE: PRT
187 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial
190      sequence of conductin protein 783-833 (dishevelled
191      homologue region)
192 <400> SEQUENCE: 5
193      Leu Thr Leu Gly His Phe Lys Glu Gln Leu Ser Lys Lys Gly Asn Tyr
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195      Arg Tyr Tyr Phe Lys Lys Ala Ser Asp Glu Phe Ala Cys Gly Ala Val
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208      <400> SEQUENCE: 6
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211      agccgattgc tgagaggaac tggaagaaga aaaaggagga ggagggaaaa aaagcaaaac 180
212      aaaatccaaa ctcaagtgaga cgctctccct caccatgagt agcgcctgtg tagtgactct 240
213      ccttccagat cccagcagca gcttccgcga ggatgctccg cggcccccggt ttccgggaga 300
214      agaaggggag accccaccgt gtcagcctag tgtgggcaag gtccagtcca ccaaacctat 360
215      gcccgtttcc tctaattgcta ggcggaatga agatggactg ggggagcccc aggggagggg 420
216      ctccccgat tcccccttga ccagggtggac caagtcttta cactccttgt tgggtgacca 480
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221      catgtttgac caggcacaga ccgagatcca ggcagtgatg gaggaaaatg cctaccaggt 780
222      gttcttgact tctgacattt acctggaata tgtgaggagt gggggggaaa acacagctta 840
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**VERIFICATION SUMMARY**  
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